

SEQUENCE LISTING

<110> Fuso Pharmaceutical Industries Ltd.

<120> Novel serine protease BSSP5

5 <130> 661640

<150> JP 10-347806

<151> 1998-11-20

<160> 32

10 <210> 1

<211> 1149

<212> DNA

<213> human

15 <400> 1

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atg ttg ctg ctc agc ctg acc cta agc ctg gtt ctc ctc ggc tcc tcc 58

Met Leu Leu Leu Ser Leu Thr Leu Ser Leu Val Leu Leu Gly Ser Ser

-30

-25

-20

20 tgg ggc tgc ggc att cct gcc atc aaa ccg gca ctg agc ttc agc cag agg 109

Trp Gly Cys Gly Ile Pro Ala Ile Lys Pro Ala Leu Ser Phe Ser Gln Arg

-15

-10

-5

-1

att gtc aac ggg gag aat gca gtg ttg ggc tcc tgg ccc tgg cag gtg tcc 160

Ile Val Asn Gly Glu Asn Ala Val Leu Gly Ser Trp Pro Trp Gln Val Ser

25

1

5

10

15

09856319.052101

ctg cag gac agc agc ggc ttc cac ttc tgc ggt ggt tct ctc atc agc cag 211

Leu Gln Asp Ser Ser Gly Phe His Phe Cys Gly Gly Ser Leu Ile Ser Gln

20

25

30

tcc tgg gtg gtc act gct gcc cac tgc aat gtc agc cct ggc cgc cat ttt 262

5 Ser Trp Val Val Thr Ala Ala His Cys Asn Val Ser Pro Gly Arg His Phe

35

40

45

50

gtt gtc ctg ggc gag tat gac cga tca tca aac gca gag ccc ttg cag gtt 313

Val Val Leu Gly Glu Tyr Asp Arg Ser Ser Asn Ala Glu Pro Leu Gln Val

55

60

65

10 ctg tcc gtc tct cgg gcc att aca cac cct agc tgg aac tct acc acc atg 364

Leu Ser Val Ser Arg Ala Ile Thr His Pro Ser Trp Asn Ser Thr Thr Met

70

75

80

85

aac aat gac gtg acg ctg ctg aag ctc gcc tcg cca gcc cag tac aca aca 415

Asn Asn Asp Val Thr Leu Leu Lys Leu Ala Ser Pro Ala Gln Tyr Thr Thr

15 90 95 100

cgc atc tcg cca gtt tgc ctg gca tcc tca aac gag gct ctg act gaa ggc 466

Arg Ile Ser Pro Val Cys Leu Ala Ser Ser Asn Glu Ala Leu Thr Glu Gly

105

110

115

ctc acg tgt gtc acc acc ggc tgg ggt cgc ctc agt ggc gtg ggc aat gtg 517

20 Leu Thr Cys Val Thr Thr Gly Trp Gly Arg Leu Ser Gly Val Gly Asn Val

120

125

130

135

aca cca gca cat ctg cag cag gtg gct ttg ccc ctg gtc act gtg aat cag 568

Thr Pro Ala His Leu Gln Gln Val Ala Leu Pro Leu Val Thr Val Asn Gln

140

145

150

25 tgc cgg cag tac tgg gac tca agt atc act gac tcc atg atc tgt gca ggt 619

09856319-052101
TOT250-6TE95960

Cys Arg Gln Tyr Trp Asp Ser Ser Ile Thr Asp Ser Met Ile Cys Ala Gly

155 160 165 170

ggc gca ggt gcc tcc tgc tgc cag ggt gac tcc gga ggc cct ctt gtc tgc 670

Gly Ala Gly Ala Ser Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys

5 175 180 185

cag aag gga aac aca tgg gtg ctt att ggt att gtc tcc tgg ggc acc aaa 721

Gln Lys Gly Asn Thr Trp Val Leu Ile Gly Ile Val Ser Trp Gly Thr Lys

190 195 200

aac tgc aat gtg cgc gca cct gct gtg tat act cga gtt agc aag ttc agc 772

10 Asn Cys Asn Val Arg Ala Pro Ala Val Tyr Thr Arg Val Ser Lys Phe Ser

205 210 215 220

acc tgg atc aac cag gtc ata gcc tac aac tga gctcaccaca ggccctcccc 825

Thr Trp Ile Asn Gln Val Ile Ala Tyr Asn

225 230

15 agctcaaccc atttaaagga cccaggccct gtcccatcat gcattcatgt ctgtcttcct 885

ggctcaggag aaagaagagg ctgttgaggg tccgactccc tacttggact tctggcacag 945

aaggggctga gtgactcctt gagtagcagt ggctcttcct agagtagcca tgccgtggcc 1005

ggggccccca cccctcctcc agggcaaccc cttggtccta cagcaagaag ccagaactgt 1065

tggaatgaat ggcagccctc cttggagagg cagcctgttt actgaatata gaggatacgt 1125

20 ttacaaaaaa aaaaaaaaaa aaaa 1149

<210> 2

<211> 264

<212> PRT

25 <213> human

09856310.052101

<400> 2

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-30

-25

-20

5 Trp Gly Cys Gly Ile Pro Ala Ile Lys Pro Ala Leu Ser Phe Ser Gln Arg

-15

-10

-5

-1

Ile Val Asn Gly Glu Asn Ala Val Leu Gly Ser Trp Pro Trp Gln Val Ser

1

5

10

15

Leu Gln Asp Ser Ser Gly Phe His Phe Cys Gly Gly Ser Leu Ile Ser Gln

10

20

25

30

Ser Trp Val Val Thr Ala Ala His Cys Asn Val Ser Pro Gly Arg His Phe

35

40

45

50

Val Val Leu Gly Glu Tyr Asp Arg Ser Ser Asn Ala Glu Pro Leu Gln Val

55

60

65

15

Leu Ser Val Ser Arg Ala Ile Thr His Pro Ser Trp Asn Ser Thr Thr Met

70

75

80

85

Asn Asn Asp Val Thr Leu Leu Lys Leu Ala Ser Pro Ala Gln Tyr Thr Thr

90

95

100

Arg Ile Ser Pro Val Cys Leu Ala Ser Ser Asn Glu Ala Leu Thr Glu Gly

20

105

110

115

Leu Thr Cys Val Thr Thr Gly Trp Gly Arg Leu Ser Gly Val Gly Asn Val

120

125

130

135

Thr Pro Ala His Leu Gln Gln Val Ala Leu Pro Leu Val Thr Val Asn Gln

140

145

150

25

Cys Arg Gln Tyr Trp Asp Ser Ser Ile Thr Asp Ser Met Ile Cys Ala Gly

09856319.052101

155 160 165 170
Gly Ala Gly Ala Ser Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys

175 180 185
Gln Lys Gly Asn Thr Trp Val Leu Ile Gly Ile Val Ser Trp Gly Thr Lys

5 190 195 200
Asn Cys Asn Val Arg Ala Pro Ala Val Tyr Thr Arg Val Ser Lys Phe Ser

205 210 215 220
Thr Trp Ile Asn Gln Val Ile Ala Tyr Asn

225 230

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<210> 3

<211> 834

<212> DNA

<213> mouse

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<400> 3

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Met Leu Leu Leu Ser Leu Thr Leu

-30

20 agc ctg gtc ctc ctt ggc tcc tcc tgg ggc tgt ggt gtt cct gcc atc acg 107

Ser Leu Val Leu Leu Gly Ser Ser Trp Gly Cys Gly Val Pro Ala Ile Thr

-25 -20 -15 -10

cct gca ctg agc tac aat cag aga att gtc aac ggg gag aat gca gtg cca 158

Pro Ala Leu Ser Tyr Asn Gln Arg Ile Val Asn Gly Glu Asn Ala Val Pro

25

-5

-1 1

5

09856319.052101
TOT250" 6TE95860

ggc tcc tgg ccc tgg cag gtg tct ctc cag gat aac acc ggc ttc cac ttc 209

Gly Ser Trp Pro Trp Gln Val Ser Leu Gln Asp Asn Thr Gly Phe His Phe

10 15 20 25

tgc ggt ggt tct ctc atc agt ccg aac tgg gtg gtc acg gct gcc cac tgc 260

5 Cys Gly Gly Ser Leu Ile Ser Pro Asn Trp Val Val Thr Ala Ala His Cys

30 35 40

caa gtc acg cct gga cgc cac ttt gtc gtt ttg gga gaa tat gac cga tct 311

Gln Val Thr Pro Gly Arg His Phe Val Val Leu Gly Glu Tyr Asp Arg Ser

45 50 55 60

10 tcc aat gct gaa cct gtg cag gtc ctc tcg atc gca agg gcc atc aca cac 362

Ser Asn Ala Glu Pro Val Gln Val Leu Ser Ile Ala Arg Ala Ile Thr His

65 70 75

cct aac tgg aac gcc aac acc atg aac aat gac ctg act ctc ctg aag ctt 413

Pro Asn Trp Asn Ala Asn Thr Met Asn Asn Asp Leu Thr Leu Leu Lys Leu

15 80 85 90

gcc tcg cca gcc cgg tac aca gca caa gtc tca cca gtc tgc ctg gct tcc 464

Ala Ser Pro Ala Arg Tyr Thr Ala Gln Val Ser Pro Val Cys Leu Ala Ser

95 100 105 110

aca aac gag gca ctg cct tcg ggg ctc acc tgt gtc acc act ggc tgg ggc 515

20 Thr Asn Glu Ala Leu Pro Ser Gly Leu Thr Cys Val Thr Thr Gly Trp Gly

115 120 125

cga atc agt ggt gtg ggc aat gtg aca cca gct cgc ctg cag caa gtt gtt 566

Arg Ile Ser Gly Val Gly Asn Val Thr Pro Ala Arg Leu Gln Gln Val Val

130 135 140 145

25 cta ccc ctg gtc act gtg aat cag tgt cgg cag tac tgg ggt gca cgc att 617

0955319-05404

Leu Pro Leu Val Thr Val Asn Gln Cys Arg Gln Tyr Trp Gly Ala Arg Ile

150

155

160

acc gat gcc atg ata tgt gca ggt ggc tca ggc gcc tcc tca tgt cag ggt 668

Thr Asp Ala Met Ile Cys Ala Gly Gly Ser Gly Ala Ser Ser Cys Gln Gly

5

165

170

175

gac tca gga ggc cct ctt gtc tgc cag aag gga aac acc tgg gtg ctt att 719

Asp Ser Gly Gly Pro Leu Val Cys Gln Lys Gly Asn Thr Trp Val Leu Ile

180

185

190

195

ggg att gtc tcc tgg ggc act aag aac tgc aac ata caa gca ccg gcc atg 770

10

Gly Ile Val Ser Trp Gly Thr Lys Asn Cys Asn Ile Gln Ala Pro Ala Met

200

205

210

tac act cgg gtc agc aag ttc agt acc tgg atc aac caa gtc atg gcc tac 821

Tyr Thr Arg Val Ser Lys Phe Ser Thr Trp Ile Asn Gln Val Met Ala Tyr

215

220

225

230

15

aac taaactgtcc

834

Asn

<210> 4

<211> 264

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<212> PRT

<213> mouse

<400> 4

Met Leu Leu Leu Ser Leu Thr Leu

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Ser Leu Val Leu Leu Gly Ser Ser Trp Gly Cys Gly Val Pro Ala Ile Thr

-25 -20 -15 -10

Pro Ala Leu Ser Tyr Asn Gln Arg Ile Val Asn Gly Glu Asn Ala Val Pro

-5 -1 1 5

5 Gly Ser Trp Pro Trp Gln Val Ser Leu Gln Asp Asn Thr Gly Phe His Phe

10 15 20 25

Cys Gly Gly Ser Leu Ile Ser Pro Asn Trp Val Val Thr Ala Ala His Cys

30 35 40

Gln Val Thr Pro Gly Arg His Phe Val Val Leu Gly Glu Tyr Asp Arg Ser

10 45 50 55 60

Ser Asn Ala Glu Pro Val Gln Val Leu Ser Ile Ala Arg Ala Ile Thr His

65 70 75

Pro Asn Trp Asn Ala Asn Thr Met Asn Asn Asp Leu Thr Leu Leu Lys Leu

80 85 90

15 Ala Ser Pro Ala Arg Tyr Thr Ala Gln Val Ser Pro Val Cys Leu Ala Ser

95 100 105 110

Thr Asn Glu Ala Leu Pro Ser Gly Leu Thr Cys Val Thr Thr Gly Trp Gly

115 120 125

Arg Ile Ser Gly Val Gly Asn Val Thr Pro Ala Arg Leu Gln Gln Val Val

20 130 135 140 145

Leu Pro Leu Val Thr Val Asn Gln Cys Arg Gln Tyr Trp Gly Ala Arg Ile

150 155 160

Thr Asp Ala Met Ile Cys Ala Gly Gly Ser Gly Ala Ser Ser Cys Gln Gly

165 170 175

25 Asp Ser Gly Gly Pro Leu Val Cys Gln Lys Gly Asn Thr Trp Val Leu Ile

00856319-052101

180 185 190 195
 Gly Ile Val Ser Trp Gly Thr Lys Asn Cys Asn Ile Gln Ala Pro Ala Met
 200 205 210
 Tyr Thr Arg Val Ser Lys Phe Ser Thr Trp Ile Asn Gln Val Met Ala Tyr
 5 215 220 225 230

Asn

<210> 5

<211> 99

10 <212> DNA

<213> Artificial Sequence

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<223> Designed oligonucleotide to construct plasmid pSecTrypHis

15 <400> 5

aagcttggct agcaacacca tgaatctact cctgatacctt acctttgttg ctgctgctgt 60 tgctgcccc
 tttgacgacg atgacaagga tccgaattc 99

<210> 6

20 <211> 99

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide to construct plasmid pSecTrypHis

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09855319-052104
 707250-6799860

<400> 6

gaattcggat ccttgtcatc gtcgtcaaag ggggcagcaa cagcagcagc aacaaaggta 60 aggatcagga
gtagattcat ggtgttgcta gccaaagctt 99

5 <210> 7

<211> 15

<212> DNA

<213> Artificial Sequence

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10 <223> Designed oligonucleotide primer to amplify neurosin-encoding sequence

<400> 7

ttggtgcatg gcgga 15

15 <210> 8

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

20 <223> Designed oligonucleotide primer to amplify neurosin-encoding sequence

<400> 8

tcctcgagac ttggcctgaa tggtttt 27

25 <210> 9

09856319.052101
TOT250" 6TE9860

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

5 <223> Designed oligonucleotide primer to amplify a portion of plasmid
pSecTrypHis/Neurosin

<400> 9

gcgctagcag atctccatga atctactcct gatcc

35

10

<210> 10

<211> 29

<212> DNA

<213> Artificial Sequence

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<220>

<223> Designed oligonucleotide primer to amplify a portion of plasmid
pSecTrypHis/Neurosin

<400> 10

20

tgaagcttgc catggaccaa cttgtcatc

29

<210> 11

<211> 26

<212> DNA

25

<213> Artificial Sequence

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<220>

<223> Designed oligonucleotide primer to amplify a portion of plasmid pTrypHis

<400> 11

5 ccaagcttca ccatcaccat caccat

26

<210> 12

<211> 17

<212> DNA

10 <213> Artificial Sequence

<220>

<223> Designed oligonucleotide primer to amplify a portion of plasmid
pTrypSigTag

15 <400> 12

gcacagtcga ggctgat

17

<210> 13

<211> 17

20 <212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide primer to amplify a portion of plasmid
pFBTrypSigTag

25

09855319.052101
TOT250"6TE95960

<400> 13

caaatgtggt atggctg

17

<210> 14

5 <211> 20

<212> DNA

<213> Artificial Sequence

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10 <223> Designed oligonucleotide primer to amplify conserved region of serin
proteases-encoding sequence

<220>

<221> UNSURE

<220> 9, 12

15 <223> n is a, c, g or t.

<400> 14

gtgctcacng cngcbcaytg

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<210> 15

20 <211> 20

<212> DNA

<213> Artificial Sequence

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25 <223> Designed oligonucleotide primer to amplify conserved region of serin
proteases-encoding sequence

09856319.052101
TOT250"6TC95860

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<220> 12, 15

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<400> 15

ccvctrwsdc cncnggcga

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<210> 16

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<211> 20

<212> DNA

<213> Artificial Sequence

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<223> Designed oligonucleotide primer for RACE for hBSP5 (forward)

15

<400> 16

tgtcagccct ggccgccatt

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<210> 17

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<211> 20

<212> DNA

<213> Artificial Sequence

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<223> Designed oligonucleotide primer for RACE for hBSP5 (forward)

25

09856319.052101

<400> 17

gcgagtatga ccgatcatca

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<210> 18

5 <211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide primer for RACE for hBSP5 (reverse)

10

<400> 18

cgccacctgc acagatcatg

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<210> 19

15 <211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide primer for RACE for hBSP5 (reverse)

20

<400> 19

gaatcagtgc cggcagtact

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<210> 20

25 <211> 20

00856319.052101

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide primer designated as hBSSP5F1 to amplify full

5 length hBSSP5 (forward)

<400> 20

tgccacgatg ttgctgctca

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10 <210> 21

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

15 <223> Designed oligonucleotide primer designated as hBSSP5F2 to amplify mature
hBSSP5-encoding region (forward)

<400> 21

attgtcaacg gggagaatgc

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<210> 22

<211> 27

<212> DNA

<213> Artificial Sequence

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T0T250.6T25860

<223> Designed oligonucleotide primer designated as hBSSP5R1/E to amplify full length hBSSP5 (reverse)

<400> 22

5 ggaattcggg tctttaatgg gttgagc

27

<210> 23

<211> 18

<212> DNA

10 <213> Artificial Sequence

<220>

<223> Designed oligonucleotide primer designated as hBSSP5R4 for RT-PCR (reverse)

15 <400> 23

cctggcacga ggaggcac

18

<210> 24

<211> 20

20 <212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide primer designated as mBSSP5F1 for RACE for mBSSP5 (forward)

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09855319.052101
T01250" 6TE95860

<400> 24

accatgaaca atgacctgac

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<210> 25

5 <211> 17

<212> DNA

<213> Artificial Sequence

<220>

10 <223> Designed oligonucleotide primer designated as mBSSP5F2 for RACE for mBSSP5
(forward)

<400> 25

gaatcagtgt cggcagt

17

15 <210> 26

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

20 <223> Designed oligonucleotide primer designated as mBSSP5F3 to amplify full
length mBSSP5 (forward)

<400> 26

gaccatctca acaccattcc

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25

09356319.052101
TOT250" STESS80

<210> 27

<211> 20

<212> DNA

<213> Artificial Sequence

5 <220>

<223> Designed oligonucleotide primer designated as mBSSP5Fmature to amplify mature mBSSP5-encoding region (forward)

<400> 27

10 attgtcaacg gggagaatgc

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<210> 28

<211> 20

<212> DNA

15 <213> Artificial Sequence

<220>

<223> Designed oligonucleotide primer designated as mBSSP5.1 for RACE for mBSSP5 (reverse)

20 <400> 28

atggcatcgg taatgcgtgc

20

<210> 29

<211> 20

25 <212> DNA

09856319.052101

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide primer designated as mBSSP5R2 for RACE for mBSSP5
(reverse)

5

<400> 29

caggtgtttc ccttctggca

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<210> 30

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<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide primer designated as mBSSP5R3/E to amplify full
length mBSSP5 (reverse)

15

<400> 30

ggaattcgga cagtttagtt gtaggcc

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20

<210> 31

<211> 117

<212> DNA

<213> Artificial Sequence

<220>

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<223> Designed oligonucleotide to construct plasmid pTrypHis

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<400> 31

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tgctgcccc tttcaccatc accatcacca tgacgacgat gacaaggatc cgaattc 117

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<210> 32

<211> 117

<212> DNA

<213> Artificial Sequence

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<220>

<223> Designed oligonucleotide to construct plasmid pTrypHis

<400> 32

gaattcggat ccttgatcgc gtcgcatggt tgatggtgat ggtgaaagg ggcagcaaca 60

15

gcagcagcaa caaaggtaag gatcaggagt agattcatgg tgttgctagc caagctt 117

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TOT250" 6T293860